

# SEQUENCE LISTING

<110> Cincinnati Children's Hospital Medical Center  
Robbins, Jeffrey

<120> A ROBUST, INDUCIBLE CARDIAC PREFERRED  
EXPRESSION SYSTEM FOR TRANSGENESIS

<130> CHM02 GN053

<150> 60/393,525

<151> 2002-07-03

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5735

<212> DNA

<213> Artificial Sequence

<220>

<223> Inducible Cardiac preferred promoter

<400> 1

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```

```

<210> 2
<211> 12
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Sequence inserted in promoter.

```

```

<400> 2
tgcatgccct ga 12

```

```

<210> 3
<211> 12
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Sequence excised from promoter.

```

```

<400> 3
tatctgcca tc 12

```

```

<210> 4
<211> 42
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Sequence inserted into promoter with TetO binding
sites.

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```

<400> 4
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```

```

<210> 5
<211> 627
<212> DNA
<213> Mus musculus

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```

<220>
<221> CDS
<222> (21) ... (602)
<223> ELC1-a

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<400> 5

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Met Pro Pro Lys Lys Pro Glu Pro Lys Lys Glu

1 5 10

act gcc aag ccg gct gca gcc cct gct cca gct gca tcc gca gct ccg 101  
Thr Ala Lys Pro Ala Ala Ala Pro Ala Ala Ser Ala Ala Pro

15 20 25

gag ccc ctc aag gac tct gcc ttt gac cca aag agt gtg aag ata gac 149  
Glu Pro Leu Lys Asp Ser Ala Phe Asp Pro Lys Ser Val Lys Ile Asp

30 35 40

ttc agt gct gac cag atc gaa gaa ttc aaa gag gcc ttt tca ttg ttt 197  
Phe Ser Ala Asp Gln Ile Glu Glu Phe Lys Glu Ala Phe Ser Leu Phe

45 50 55

gac cgg act cca acg gga gag atg aag atc acc tac ggg cag tgt ggg 245  
Asp Arg Thr Pro Thr Gly Glu Met Lys Ile Thr Tyr Gly Gln Cys Gly

60 65 70 75

gac gtg ctg cgg gcc ctg ggc cag aac ccc acc aac gca gag gtg ctg 293  
Asp Val Leu Arg Ala Leu Gly Gln Asn Pro Thr Asn Ala Glu Val Leu

80 85 90

cgc gtt ttg ggc aaa ccc aag cct gaa gag atg agt tcc aag aca ctg 341  
Arg Val Leu Gly Lys Pro Lys Pro Glu Glu Met Ser Ser Lys Thr Leu

95 100 105

gac ttc gag atg ttc ctg ccc atc ctg caa cac atc tcc cgc aac aag 389  
Asp Phe Glu Met Phe Leu Pro Ile Leu Gln His Ile Ser Arg Asn Lys

110 115 120

gag cag ggc acc tat gag gac ttc gtg gag ggg ctg cgg gtc ttt gac 437  
Glu Gln Gly Thr Tyr Glu Asp Phe Val Glu Gly Leu Arg Val Phe Asp

125 130 135

aaa gaa agc aac ggc aca gtc atg ggt gcc gag ctt cgg cat gtc ctt 485  
Lys Glu Ser Asn Gly Thr Val Met Gly Ala Glu Leu Arg His Val Leu

140 145 150 155

gcc acc ctg gga gag aag atg agc gag gca gag gtg gag cag ctg ttg 533  
Ala Thr Leu Gly Glu Lys Met Ser Glu Ala Glu Val Glu Gln Leu Leu

160 165 170

tct ggg cag gag gat gcc aat ggc tgc atc aac tat gaa gcc ttt gtc 581  
Ser Gly Gln Glu Asp Ala Asn Gly Cys Ile Asn Tyr Glu Ala Phe Val

175 180 185

aag cac atc atg tct ggg taa agcacgtttc tccaggggtgg tcgac 627  
Lys His Ile Met Ser Gly \*

190

<210> 6

<211> 193

<212> PRT

{W0008878.1}

<213> Mus musculus

<400> 6

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          20          25          30
Ser Ala Phe Asp Pro Lys Ser Val Lys Ile Asp Phe Ser Ala Asp Gln
          35          40          45
Ile Glu Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Arg Thr Pro Thr
          50          55          60
Gly Glu Met Lys Ile Thr Tyr Gly Gln Cys Gly Asp Val Leu Arg Ala
65          70          75          80
Leu Gly Gln Asn Pro Thr Asn Ala Glu Val Leu Arg Val Leu Gly Lys
          85          90          95
Pro Lys Pro Glu Glu Met Ser Ser Lys Thr Leu Asp Phe Glu Met Phe
          100          105          110
Leu Pro Ile Leu Gln His Ile Ser Arg Asn Lys Glu Gln Gly Thr Tyr
          115          120          125
Glu Asp Phe Val Glu Gly Leu Arg Val Phe Asp Lys Glu Ser Asn Gly
          130          135          140
Thr Val Met Gly Ala Glu Leu Arg His Val Leu Ala Thr Leu Gly Glu
          145          150          155          160
Lys Met Ser Glu Ala Glu Val Glu Gln Leu Leu Ser Gly Gln Glu Asp
          165          170          175
Ala Asn Gly Cys Ile Asn Tyr Glu Ala Phe Val Lys His Ile Met Ser
          180          185          190
Gly
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<210> 7

<211> 1503

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (33)...(1295)

<223> GSK-CA

<400> 7

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                               Met Ser Gly Arg Pro Arg Thr
                               1          5

acc gcg ttt gcg gag agc tgc aag cca gtg cag cag cct tca gct ttt 101
Thr Ala Phe Ala Glu Ser Cys Lys Pro Val Gln Gln Pro Ser Ala Phe
          10          15          20

ggt agc atg aaa gtt agc aga gat aaa gat ggc agc aag gta acc aca 149
Gly Ser Met Lys Val Ser Arg Asp Lys Asp Gly Ser Lys Val Thr Thr
          25          30          35

gta gtg gca act cct ggc cag ggt cct gac agg cca cag gaa gtc agt 197
Val Val Ala Thr Pro Gly Gln Gly Pro Asp Arg Pro Gln Glu Val Ser
          40          45          50          55
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{W0008878.1}

tat aca gac acg aaa gtg att gga aat gga tca ttt ggt gtg gta tat	245
Tyr Thr Asp Thr Lys Val Ile Gly Asn Gly Ser Phe Gly Val Val Tyr	
60 65 70	
caa gcc aaa ctt tgt gat tct gga gaa ctg gtt gcc atc aag aaa gtt	293
Gln Ala Lys Leu Cys Asp Ser Gly Glu Leu Val Ala Ile Lys Lys Val	
75 80 85	
cta cag gac aag cga ttt aag aac cga gag ctc cag atc atg aga aag	341
Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met Arg Lys	
90 95 100	
cta gac cac tgt aac ata gtc cga ctg cgg tat ttc ttc tac tcg agt	389
Leu Asp His Cys Asn Ile Val Arg Leu Arg Tyr Phe Phe Tyr Ser Ser	
105 110 115	
ggt gag aag aaa gat gag gtc tac ctt aac ctg gtg ctg gac tat gtt	437
Gly Glu Lys Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Asp Tyr Val	
120 125 130 135	
ccg gag aca gtg tac aga gtc gcc aga cac tat agt cga gcc aag cag	485
Pro Glu Thr Val Tyr Arg Val Ala Arg His Tyr Ser Arg Ala Lys Gln	
140 145 150	
aca ctc cct gtg atc tat gtc aag ttg tat atg tat cag ctg ttc aga	533
Thr Leu Pro Val Ile Tyr Val Lys Leu Tyr Met Tyr Gln Leu Phe Arg	
155 160 165	
agt cta gcc tat atc cat tcc ttt gga atc tgc cat cga gac att aaa	581
Ser Leu Ala Tyr Ile His Ser Phe Gly Ile Cys His Arg Asp Ile Lys	
170 175 180	
cca cag aac ctc ttg ttg gat cct gat aca gct gta tta aaa ctc tgt	629
Pro Gln Asn Leu Leu Leu Asp Pro Asp Thr Ala Val Leu Lys Leu Cys	
185 190 195	
gac ttt gga agt gca aag cag ctg gtc cga gga gag ccc aat gtt tca	677
Asp Phe Gly Ser Ala Lys Gln Leu Val Arg Gly Glu Pro Asn Val Ser	
200 205 210 215	
tat atc tgt tct cgg tac tac agg gca cca gag ttg atc ttt gga gcc	725
Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe Gly Ala	
220 225 230	
act gat tac acg tcc agt ata gat gta tgg tct gca ggc tgt gtg ttg	773
Thr Asp Tyr Thr Ser Ser Ile Asp Val Trp Ser Ala Gly Cys Val Leu	
235 240 245	
gct gaa ttg ttg cta gga caa cca ata ttt cct ggg gac agt ggt gtg	821
Ala Glu Leu Leu Leu Gly Gln Pro Ile Phe Pro Gly Asp Ser Gly Val	
250 255 260	
gat cag ttg gtg gaa ata ata aag gtc cta gga aca cca aca agg gag	869
Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr Arg Glu	
265 270 275	

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Gln Ile Arg Glu Met Asn Pro Asn Tyr Thr Glu Phe Lys Phe Pro Gln
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atc aag gca cat cct tgg aca aag gtc ttc cgg ccc cga act cca cca 965
Ile Lys Ala His Pro Trp Thr Lys Val Phe Arg Pro Arg Thr Pro Pro
300                305                310

gag gca att gca ctg tgc agc cgt ctg ctg gag tac aca cct acc gcc 1013
Glu Ala Ile Ala Leu Cys Ser Arg Leu Leu Glu Tyr Thr Pro Thr Ala
315                320                325

cgg cta aca cca ctg gaa gct tgt gca cat tca ttt ttc gat gaa ttg 1061
Arg Leu Thr Pro Leu Glu Ala Cys Ala His Ser Phe Phe Asp Glu Leu
330                335                340

cgg gac cca aat gtc aaa cta cca aat ggg cga gac aca cct gca ctc 1109
Arg Asp Pro Asn Val Lys Leu Pro Asn Gly Arg Asp Thr Pro Ala Leu
345                350                355

ttc aac ttt acc act caa gaa ctg tca agt aac ccc cct ctg gcc acc 1157
Phe Asn Phe Thr Thr Gln Glu Leu Ser Ser Asn Pro Pro Leu Ala Thr
360                365                370                375

atc ctt atc cct cca cat gct cgg att cag gcc gct gct tca ccg cct 1205
Ile Leu Ile Pro Pro His Ala Arg Ile Gln Ala Ala Ala Ser Pro Pro
380                385                390

gcc aac gcc aca gca gcc tca gat act aat gct gga gac cgt gga cag 1253
Ala Asn Ala Thr Ala Ala Ser Asp Thr Asn Ala Gly Asp Arg Gly Gln
395                400                405

acc aat aac gcc gct tct gca tca gct tcc aac tcc acc tga 1295
Thr Asn Asn Ala Ala Ser Ala Ser Ala Ser Asn Ser Thr *
410                415                420

acagcccca ggagccagct gcgcgggaaa gaccagcact tacttgagtg ccactcagca 1355
aacttggtca cgtttggaata gaaaattaaa aagaggaaaa caaaaacaaa aacaaaaaaa 1415
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<210> 8

<211> 420

<212> PRT

<213> Mus musculus

<400> 8

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20     25     30
Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
35     40     45
Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
50     55     60
Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
65     70     75     80

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{W0008878.1}

Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg  
                     85                    90                    95  
 Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu  
                     100                    105                    110  
 Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu  
                     115                    120                    125  
 Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg  
                     130                    135                    140  
 His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu  
 145                    150                    155                    160  
 Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly  
                     165                    170                    175  
 Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp  
                     180                    185                    190  
 Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val  
                     195                    200                    205  
 Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala  
                     210                    215                    220  
 Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val  
 225                    230                    235                    240  
 Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Gly Gln Pro Ile  
                     245                    250                    255  
 Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val  
                     260                    265                    270  
 Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr  
                     275                    280                    285  
 Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val  
                     290                    295                    300  
 Phe Arg Pro Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu  
 305                    310                    315                    320  
 Leu Glu Tyr Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala  
                     325                    330                    335  
 His Ser Phe Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn  
                     340                    345                    350  
 Gly Arg Asp Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser  
                     355                    360                    365  
 Ser Asn Pro Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile  
                     370                    375                    380  
 Gln Ala Ala Ala Ser Pro Pro Ala Asn Ala Thr Ala Ala Ser Asp Thr  
 385                    390                    395                    400  
 Asn Ala Gly Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala  
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 Ser Asn Ser Thr  
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ag 62